

# SCORE Search Results Details for Application 10751380 and Search Result us-10-751-380-22.p2n.rnpbn.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10751380 and Search Result us-10-751-380-22.p2n.rnpbn.

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GenCore version 5.1.8  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 25, 2006, 23:54:22 ; Search time 26 Seconds  
(without alignments)  
2657.125 Million cell updates/sec

Title: US-10-751-380-22  
Perfect score: 2077  
Sequence: 1 EFGRKKRRQRMALLRRPTVS .....IPQLNSKAVKDLASPLIGRS 408

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10751380/runat\_25052006\_104515\_19851/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss08  
-USER=US10751380\_@CGN\_1\_1\_17\_@runat\_25052006\_104515\_19851 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA\_New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	2025	97.5	1530	6	US-10-505-928-198	Sequence 198, App
2	1028	49.5	1452	6	US-10-505-928-318	Sequence 318, App
3	546	26.3	1473	7	US-11-217-529-2706	Sequence 2706, Ap
4	536.5	25.8	1425	7	US-11-217-529-997	Sequence 997, App
5	530.5	25.5	1284	7	US-11-217-529-75842	Sequence 75842, A
6	514	24.7	1287	7	US-11-217-529-347	Sequence 347, App
7	513	24.7	1833	6	US-10-953-349-13178	Sequence 13178, A
8	503.5	24.2	975	7	US-11-217-529-80034	Sequence 80034, A
9	491	23.6	954	7	US-11-217-529-4737	Sequence 4737, Ap
10	475.5	22.9	1743	7	US-11-145-307A-42	Sequence 42, Appl
11	437	21.0	1518	6	US-10-953-349-14536	Sequence 14536, A
12	424	20.4	1682	6	US-10-505-928-364	Sequence 364, App
13	414	19.9	1308	7	US-11-217-529-79016	Sequence 79016, A
14	397.5	19.1	1143	7	US-11-217-529-4165	Sequence 4165, Ap
15	394	19.0	1143	7	US-11-217-529-76758	Sequence 76758, A
16	387	18.6	1272	7	US-11-217-529-3381	Sequence 3381, Ap
17	325	15.6	1047	7	US-11-217-529-81613	Sequence 81613, A
18	315	15.2	1032	7	US-11-217-529-82400	Sequence 82400, A
19	268.5	12.9	2536	6	US-10-505-928-138	Sequence 138, App
20	196.5	9.5	1256	7	US-11-242-111-8	Sequence 8, Appli
21	165	7.9	2017	6	US-10-953-349-6624	Sequence 6624, Ap
22	156	7.5	1226	6	US-10-953-349-9694	Sequence 9694, Ap
23	156	7.5	1596	6	US-10-953-349-22736	Sequence 22736, A
24	135	6.5	1890	6	US-10-511-937-662	Sequence 662, App
25	134.5	6.5	1178	6	US-10-953-349-17819	Sequence 17819, A
26	133.5	6.4	1433	6	US-10-953-349-36654	Sequence 36654, A
27	118	5.7	3108	7	US-11-217-529-3521	Sequence 3521, Ap
28	115	5.5	1740	7	US-11-217-529-40	Sequence 40, Appl
29	113	5.4	1011	7	US-11-217-529-81248	Sequence 81248, A
30	111	5.3	4368	7	US-11-217-529-80559	Sequence 80559, A
31	108	5.2	1743	7	US-11-217-529-75355	Sequence 75355, A
32	105.5	5.1	3210	7	US-11-217-529-2695	Sequence 2695, Ap
33	101	4.9	5217	7	US-11-217-529-5142	Sequence 5142, Ap
34	100	4.8	1632	6	US-10-953-349-22593	Sequence 22593, A
35	99	4.8	4962	7	US-11-217-529-76536	Sequence 76536, A
36	98.5	4.7	4119	7	US-11-217-529-77046	Sequence 77046, A
37	97.5	4.7	2241	7	US-11-293-697-1922	Sequence 1922, Ap
38	97	4.7	2245	7	US-11-293-697-881	Sequence 881, App
39	97	4.7	6714	7	US-11-217-529-82584	Sequence 82584, A
40	96	4.6	1572	7	US-11-217-529-76624	Sequence 76624, A
41	96	4.6	2256	7	US-11-217-529-170	Sequence 170, App
42	95.5	4.6	2883	7	US-11-217-529-76512	Sequence 76512, A
43	95.5	4.6	9426	7	US-11-217-529-1662	Sequence 1662, Ap

**SCORE Search Results Details for Application  
10751380 and Search Result us-10-751-380-  
22.p2n.rst.**

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

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OM protein - nucleic search, using frame plus p2n model

```
Run on:      May 25, 2006, 23:25:05 ; Search time 4733 Seconds
              (without alignments)
              7230.642 Million cell updates/sec
```

```
Title:          US-10-751-380-22
Perfect score:  2077
Sequence:       1 EFGRKKRRQRMALLRRPTVS.....IPQLNSKAVKDLASPLIGRS 408
```

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext  7.0
```

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10751380/runat_25052006_104506_19677/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10751380_@CGN_1_1_9528_@runat_25052006_104506_19677 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :      EST:*
           1:   gb est1:*
```

2: gb\_est3:\*  
 3: gb\_est4:\*  
 4: gb\_est5:\*  
 5: gb\_est6:\*  
 6: gb\_htc:\*  
 7: gb\_est2:\*  
 8: gb\_est7:\*  
 9: gb\_est8:\*  
 10: gb\_est9:\*  
 11: gb\_gss1:\*  
 12: gb\_gss2:\*  
 13: gb\_gss3:\*  
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2025	97.5	1197	14	AY417234	AY417234 Homo sapi
2	2025	97.5	1411	6	CR624496	CR624496 full-leng
3	2025	97.5	1430	6	CR606395	CR606395 full-leng
4	2025	97.5	1431	6	CR608927	CR608927 full-leng
5	2025	97.5	1452	6	CR607796	CR607796 full-leng
6	2025	97.5	1501	6	CR608686	CR608686 full-leng
7	2025	97.5	1546	6	HSM800659	AL080146 Homo sapi
8	1974	95.0	1173	14	AY417235	AY417235 Pan trogl
9	1812	87.2	1532	6	AK076122	AK076122 Mus muscu
10	1811	87.2	1197	14	AY417236	AY417236 Mus muscu
11	1789	86.1	1408	6	AK013312	AK013312 Mus muscu
12	1553.5	74.8	1036	2	BM459148	BM459148 AGENCOURT
13	1509	72.7	1023	4	BX402439	BX402439 BX402439
14	1425	68.6	1039	3	BM554412	BM554412 AGENCOURT
15	1419	68.3	1080	1	AL533824	AL533824 AL533824
c 16	1416	68.2	1060	4	BX358205	BX358205 BX358205
17	1397	67.3	925	4	BX354143	BX354143 BX354143
c 18	1395	67.2	1076	4	BX402438	BX402438 BX402438
19	1393	67.1	849	10	DR762444	DR762444 HESC4_140
20	1389	66.9	933	3	BQ439750	BQ439750 AGENCOURT
21	1388	66.8	1016	4	BX358206	BX358206 BX358206
c 22	1368	65.9	990	4	BX354142	BX354142 BX354142
23	1361	65.5	863	9	CX873350	CX873350 HESC4_79_
24	1350	65.0	814	2	BI858560	BI858560 603389017
25	1339	64.5	776	8	CN281365	CN281365 170006000
26	1336	64.3	1136	2	BM464310	BM464310 AGENCOURT
27	1334	64.2	836	8	CX164331	CX164331 HESC2_15_
28	1319	63.5	1023	2	BM455332	BM455332 AGENCOURT
29	1316.5	63.4	896	4	CB181156	CB181156 AGENCOURT
30	1313.5	63.2	1064	6	CR600767	CR600767 full-leng
31	1297	62.4	949	4	CA487455	CA487455 AGENCOURT
32	1294	62.3	863	10	DV850523	DV850523 LB0221.CR
33	1280	61.6	756	9	DR156954	DR156954 HESC2_72_
34	1265.5	60.9	950	1	AL550817	AL550817 AL550817
35	1262.5	60.8	882	4	CA980576	CA980576 AGENCOURT
36	1261.5	60.7	932	2	BI408061	BI408061 602919017
37	1257.5	60.5	999	4	BX375984	BX375984 BX375984
38	1255	60.4	984	4	BX337662	BX337662 BX337662

**SCORE Search Results Details for Application 10751380 and Search Result us-10-751-380-22.p2n.rnpbm.**

Comments /  
Suggestions

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OM protein - nucleic search, using frame plus p2n model

```
Run on:      May 25, 2006, 23:49:04 ; Search time 1580 Seconds
              (without alignments)
              4759.514 Million cell updates/sec
```

```
Title:          US-10-751-380-22
Perfect score:  2077
Sequence:       1 EFGRKKRRQRMALLRRPTVS.....IPQLNSKAVKDLASPLIGRS 408
```

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext  7.0
```

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10751380/runat_25052006_104512_19788/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10751380_CGN_1_1_1675@runat_25052006_104512_19788 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Published Applications NA Main:\*

```

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2025	97.5	1375	8	US-10-751-380-21	Sequence 21, Appl
2	2025	97.5	1507	9	US-10-723-860-2496	Sequence 2496, Ap
3	2025	97.5	1507	10	US-10-756-149-2323	Sequence 2323, Ap
4	2025	97.5	1530	7	US-10-172-118-1075	Sequence 1075, Ap
5	2025	97.5	1530	8	US-10-342-887-1075	Sequence 1075, Ap
6	2025	97.5	1530	8	US-10-751-380-1	Sequence 1, Appli
7	2025	97.5	1530	9	US-10-733-878-416	Sequence 416, App
8	2025	97.5	1530	10	US-10-848-755A-133	Sequence 133, App
9	2025	97.5	1530	12	US-10-960-414-366	Sequence 366, App
10	2025	97.5	1530	15	US-11-000-688-955	Sequence 955, App
11	2025	97.5	1532	6	US-10-116-802-165	Sequence 165, App
12	2025	97.5	2103	9	US-10-723-860-6659	Sequence 6659, Ap
13	2019	97.2	1553	3	US-09-925-301-305	Sequence 305, App
14	1996	96.1	1197	3	US-09-994-412-2	Sequence 2, Appli
15	1922.5	92.6	1526	10	US-10-450-763-9357	Sequence 9357, Ap
16	1780	85.7	1400	16	US-11-128-061-4155	Sequence 4155, Ap
17	1780	85.7	1400	16	US-11-128-049-4155	Sequence 4155, Ap
18	1780	85.7	1403	16	US-11-128-061-513	Sequence 513, App
19	1780	85.7	1403	16	US-11-128-049-513	Sequence 513, App
20	1605.5	77.3	1247	7	US-10-085-198-109	Sequence 109, App
21	1090	52.5	826	3	US-09-773-459-12	Sequence 12, Appl
22	1090	52.5	826	7	US-10-351-953-12	Sequence 12, Appl
23	1028	49.5	1452	3	US-09-954-456-695	Sequence 695, App
24	1028	49.5	1452	3	US-09-954-456-1133	Sequence 1133, Ap
25	1028	49.5	1452	3	US-09-880-107-2308	Sequence 2308, Ap
26	1028	49.5	1452	3	US-09-967-768A-145	Sequence 145, App
27	1028	49.5	1452	3	US-09-954-531-147	Sequence 147, App
28	1028	49.5	1452	3	US-09-292-758-27	Sequence 27, Appl
29	1028	49.5	1452	3	US-09-873-367C-1008	Sequence 1008, Ap
30	1028	49.5	1452	6	US-10-171-581-136	Sequence 136, App
31	1028	49.5	1452	8	US-10-641-643-1048	Sequence 1048, Ap
32	1028	49.5	1452	10	US-10-843-641A-1008	Sequence 1008, Ap
33	1028	49.5	1452	10	US-10-843-641A-1214	Sequence 1214, Ap
34	1028	49.5	1452	10	US-10-843-641A-3722	Sequence 3722, Ap
35	1028	49.5	1452	10	US-10-843-641A-4160	Sequence 4160, Ap

**SCORE Search Results Details for Application 10751380 and Search Result us-10-751-380-22.p2n.rge.**

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10751380 and Search Result us-10-751-380-22.p2n.rge.

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OM protein - nucleic search, using frame plus p2n model

```
Run on:      May 25, 2006, 23:13:14 ; Search time 6002 Seconds
              (without alignments)
              6520.463 Million cell updates/sec
```

Title: US-10-751-380-22  
Perfect score: 2077  
Sequence: 1 EFGRKKRRQRMALLRRPTVS.....IPQLNSKAVKDLASPLIGRS 408

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext  7.0
```

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10751380/runat_25052006_104504_19648/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10751380_@CGN_1_1_8328_@runat_25052006_104504_19648 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :      GenEmbl:*
           1:  gb env:*
```

2: gb\_pat:\*  
 3: gb\_ph:\*  
 4: gb\_pl:\*  
 5: gb\_pr:\*  
 6: gb\_ro:\*  
 7: gb\_sts:\*  
 8: gb\_sy:\*  
 9: gb\_un:\*  
 10: gb\_vi:\*  
 11: gb\_ov:\*  
 12: gb\_htg:\*  
 13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2025	97.5	1197	8	AY891142	AY891142 Synthetic
2	2025	97.5	1197	8	AY891143	AY891143 Synthetic
3	2025	97.5	1197	8	BT019456	BT019456 Synthetic
4	2025	97.5	1197	8	BT019457	BT019457 Synthetic
5	2025	97.5	1206	5	CR533527	CR533527 Homo sapi
6	2025	97.5	1361	5	BC105086	BC105086 Homo sapi
7	2025	97.5	1361	5	BC105112	BC105112 Homo sapi
8	2025	97.5	1375	2	AR448970	AR448970 Sequence
9	2025	97.5	1401	5	AF002822	AF002822 Human cyc
10	2025	97.5	1433	5	AB020981	AB020981 Homo sapi
11	2025	97.5	1507	2	BD156255	BD156255 Primer fo
12	2025	97.5	1507	2	AX876674	AX876674 Sequence
13	2025	97.5	1507	5	AK001404	AK001404 Homo sapi
14	2025	97.5	1530	2	CQ959726	CQ959726 Sequence
15	2025	97.5	1530	2	CQ981348	CQ981348 Sequence
16	2025	97.5	1530	2	CS031177	CS031177 Sequence
17	2025	97.5	1530	2	CS040129	CS040129 Sequence
18	2025	97.5	1530	2	CS063038	CS063038 Sequence
19	2025	97.5	1530	2	CS080819	CS080819 Sequence
20	2025	97.5	1530	2	CS118908	CS118908 Sequence
21	2025	97.5	1530	2	CS161901	CS161901 Sequence
22	2025	97.5	1530	2	AR448968	AR448968 Sequence
23	2025	97.5	1530	2	AX779987	AX779987 Sequence
24	2025	97.5	1981	2	BD106750	BD106750 Cyclin-li
25	2022	97.4	1497	5	AK222611	AK222611 Homo sapi
26	2012	96.9	1197	5	BT019458	BT019458 Homo sapi
27	2003	96.4	1502	5	AF087910	AF087910 Homo sapi
28	1988	95.7	1551	5	AB168913	AB168913 Macaca fa
29	1987	95.7	1496	5	AB169084	AB169084 Macaca fa
30	1986	95.6	1342	2	CQ726844	CQ726844 Sequence
31	1914	92.2	1465	14	BT021153	BT021153 Bos tauru
32	1909	91.9	1472	14	BT020669	BT020669 Bos tauru
33	1909	91.9	1505	14	BT020648	BT020648 Bos tauru
34	1904	91.7	1452	14	BT020822	BT020822 Bos tauru
35	1904	91.7	1454	14	BT020762	BT020762 Bos tauru
36	1903	91.6	1299	14	AF080219	AF080219 Bos tauru
37	1878.5	90.4	1399	6	HAMCYCLIN2	D17294 Mesocricetu



**SCORE Search Results Details for Application 10751380 and Search Result us-10-751-380-21.rst.**

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10751380 and Search Result us-10-751-380-21.rst.

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OM nucleic - nucleic search, using sw model

```
Run on:      May 25, 2006, 22:31:08 ; Search time 7194 Seconds
              (without alignments)
              10687.946 Million cell updates/sec
```

Title: US-10-751-380-21  
Perfect score: 1375  
Sequence: 1 gaattcgccaggaagaagcg.....cactgataggaaggctctag 1375

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
No.						
1	1345.4	97.8	1501	6	CR608686	CR608686 full-leng
2	1333	96.9	1546	6	HSM800659	AL080146 Homo sapi
3	1317	95.8	1431	6	CR608927	CR608927 full-leng
4	1309	95.2	1452	6	CR607796	CR607796 full-leng
5	1299	94.5	1430	6	CR606395	CR606395 full-leng
6	1258	91.5	1411	6	CR624496	CR624496 full-leng
7	1197	87.1	1197	14	AY417234	AY417234 Homo sapi
8	1165	84.7	1173	14	AY417235	AY417235 Pan trogl
9	974	70.8	1039	3	BM554412	BM554412 AGENCOURT
10	972.4	70.7	1080	1	AL533824	AL533824 AL533824
11	955.4	69.5	1023	4	BX402439	BX402439 BX402439
12	945.8	68.8	1532	6	AK076122	AK076122 Mus muscu
13	939.4	68.3	1197	14	AY417236	AY417236 Mus muscu
14	926.6	67.4	1408	6	AK013312	AK013312 Mus muscu
15	925	67.3	925	4	BX354143	BX354143 BX354143
16	914.4	66.5	1023	2	BM455332	BM455332 AGENCOURT
17	901.4	65.6	949	4	CA487455	CA487455 AGENCOURT
18	898	65.3	1036	2	BM459148	BM459148 AGENCOURT
19	889.2	64.7	1016	4	BX358206	BX358206 BX358206
20	888.6	64.6	999	4	BX375984	BX375984 BX375984
21	868	63.1	950	1	AL550817	AL550817 AL550817
22	863	62.8	1136	2	BM464310	BM464310 AGENCOURT
23	861.6	62.7	1018	3	BM553940	BM553940 AGENCOURT
24	856.8	62.3	863	9	CX873350	CX873350 HESC4_79_
c 25	854.8	62.2	1060	4	BX358205	BX358205 BX358205
26	846.8	61.6	984	4	BX337662	BX337662 BX337662
27	842.4	61.3	975	2	BG761038	BG761038 602717548
28	840.6	61.1	1047	2	BM455350	BM455350 AGENCOURT
29	838	60.9	849	10	DR762444	DR762444 HESC4_140
c 30	837.4	60.9	1076	4	BX402438	BX402438 BX402438
31	836	60.8	836	8	CX164331	CX164331 HESC2_15_
32	832	60.5	865	3	BQ423642	BQ423642 AGENCOURT
33	831.2	60.5	983	3	BQ065301	BQ065301 AGENCOURT
c 34	817.8	59.5	990	4	BX354142	BX354142 BX354142
35	813.8	59.2	867	1	AU143015	AU143015 AU143015
36	811.6	59.0	933	3	BQ439750	BQ439750 AGENCOURT
37	799.8	58.2	864	3	BU543842	BU543842 AGENCOURT
38	798.8	58.1	860	1	AU143555	AU143555 AU143555
39	798.2	58.1	814	2	BI858560	BI858560 603389017
40	794	57.7	822	2	BG681291	BG681291 602627140
41	781.8	56.9	953	2	BG719723	BG719723 602690448
c 42	780.6	56.8	1023	4	BX375983	BX375983 BX375983
43	779	56.7	779	9	DR155704	DR155704 HESC2_57_
44	775.6	56.4	907	3	BQ223737	BQ223737 AGENCOURT
45	774.4	56.3	776	8	CN281365	CN281365 170006000

## ALIGNMENTS

RESULT 1  
CR608686  
LOCUS

CR608686

1501 bp

mRNA

linear

HTC 21-JUL-2004

**SCORE Search Results Details for Application 10751380 and Search Result us-10-751-380-21.rnpbm.**

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10751380 and Search Result us-10-751-380-21.rnpbm.

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OM nucleic - nucleic search, using sw model

```
Run on:      May 25, 2006, 23:02:12 ; Search time 1674 Seconds
              (without alignments)
              10092.890 Million cell updates/sec
```

Title: US-10-751-380-21  
Perfect score: 1375  
Sequence: 1 qaattcqqccaggaagaagcg.....cactgataggaaggctctag 1375

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	1375	100.0		1375	8	US-10-751-380-21	Sequence 21, Appl
2	1345	97.8		1507	9	US-10-723-860-2496	Sequence 2496, Ap
3	1345	97.8		1507	10	US-10-756-149-2323	Sequence 2323, Ap
4	1345	97.8		1530	7	US-10-172-118-1075	Sequence 1075, Ap
5	1345	97.8		1530	8	US-10-342-887-1075	Sequence 1075, Ap
6	1345	97.8		1530	8	US-10-751-380-1	Sequence 1, Appli
7	1345	97.8		1530	9	US-10-733-878-416	Sequence 416, App
8	1345	97.8		1530	10	US-10-848-755A-133	Sequence 133, App
9	1345	97.8		1530	12	US-10-960-414-366	Sequence 366, App
10	1345	97.8		1530	15	US-11-000-688-955	Sequence 955, App
11	1345	97.8		2103	9	US-10-723-860-6659	Sequence 6659, Ap
12	1344.6	97.8		1553	3	US-09-925-301-305	Sequence 305, App
13	1334.4	97.0		1532	6	US-10-116-802-165	Sequence 165, App
14	1253.6	91.2		1526	10	US-10-450-763-9357	Sequence 9357, Ap
15	1190.6	86.6		1197	3	US-09-994-412-2	Sequence 2, Appli
16	959.6	69.8		1247	7	US-10-085-198-109	Sequence 109, App
17	933.8	67.9		1400	16	US-11-128-061-4155	Sequence 4155, Ap
18	933.8	67.9		1400	16	US-11-128-049-4155	Sequence 4155, Ap
19	933.8	67.9		1403	16	US-11-128-061-513	Sequence 513, App
20	933.8	67.9		1403	16	US-11-128-049-513	Sequence 513, App
21	653.6	47.5		826	3	US-09-773-459-12	Sequence 12, Appl
22	653.6	47.5		826	7	US-10-351-953-12	Sequence 12, Appl
23	459.4	33.4		638	3	US-09-879-536-186	Sequence 186, App
24	424.2	30.9		849	10	US-10-450-763-9356	Sequence 9356, Ap
25	406.8	29.6		524	10	US-10-450-763-9355	Sequence 9355, Ap
c 26	377	27.4		721	16	US-11-136-527-1072	Sequence 1072, Ap
27	361.2	26.3		2352	16	US-11-128-061-420	Sequence 420, App
28	361.2	26.3		2352	16	US-11-128-049-420	Sequence 420, App
29	359.6	26.2		1452	3	US-09-954-456-695	Sequence 695, App
30	359.6	26.2		1452	3	US-09-954-456-1133	Sequence 1133, Ap
31	359.6	26.2		1452	3	US-09-880-107-2308	Sequence 2308, Ap
32	359.6	26.2		1452	3	US-09-967-768A-145	Sequence 145, App
33	359.6	26.2		1452	3	US-09-954-531-147	Sequence 147, App
34	359.6	26.2		1452	3	US-09-292-758-27	Sequence 27, Appl
35	359.6	26.2		1452	3	US-09-873-367C-1008	Sequence 1008, Ap
36	359.6	26.2		1452	6	US-10-171-581-136	Sequence 136, App
37	359.6	26.2		1452	8	US-10-641-643-1048	Sequence 1048, Ap
38	359.6	26.2		1452	10	US-10-843-641A-1008	Sequence 1008, Ap
39	359.6	26.2		1452	10	US-10-843-641A-1214	Sequence 1214, Ap
40	359.6	26.2		1452	10	US-10-843-641A-3722	Sequence 3722, Ap
41	359.6	26.2		1452	10	US-10-843-641A-4160	Sequence 4160, Ap
42	359.6	26.2		1452	10	US-10-843-641A-6290	Sequence 6290, Ap
43	359.6	26.2		1570	6	US-10-098-841-236	Sequence 236, App
44	359.6	26.2		1578	7	US-10-388-360-292	Sequence 292, App
45	359.6	26.2		1578	8	US-10-188-832-122	Sequence 122, App

## ALIGNMENTS

RESULT 1

Comments /  
Suggestions

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1375	100.0	1375	12	ADO26480	Ado26480 Chimeric
2	1375	100.0	1375	12	ADQ60193	Adq60193 Human cyc
3	1345	97.8	1507	4	AAH14263	Aah14263 Human cDN
4	1345	97.8	1507	12	ADQ19677	Adq19677 Human sof
5	1345	97.8	1530	10	ADF81588	Adf81588 Leukaemia
6	1345	97.8	1530	11	ADN95276	Adn95276 Human BEC
7	1345	97.8	1530	12	ADO26460	Ado26460 Human cyc
8	1345	97.8	1530	12	ADN03889	Adn03889 Antipsori
9	1345	97.8	1530	12	ADQ09231	Adq09231 Human CCN
10	1345	97.8	1530	12	ADQ60173	Adq60173 Human cDN
11	1345	97.8	1530	13	ADR25214	Adr25214 Breast ca
12	1345	97.8	1530	13	ACN39816	Acn39816 Tumour-as
13	1345	97.8	1530	13	ADU05981	Adu05981 Novel bro
14	1345	97.8	1530	14	ADY14877	Ady14877 DNA encod
15	1345	97.8	1530	14	ADY61817	Ady61817 Human gen
16	1345	97.8	1530	14	ADZ09578	Adz09578 Human bre
17	1345	97.8	1530	14	AEC82574	Aec82574 Breast ca
18	1345	97.8	1530	14	AEC75991	Aec75991 Genetic m
19	1345	97.8	1530	15	AEE84832	Aee84832 IMPDH mar
20	1345	97.8	2103	12	ADQ23839	Adq23839 Human sof
21	1344.6	97.8	1553	3	AAC77911	Aac77911 Human can
22	1334.4	97.0	1532	9	ACH03960	Ach03960 Human cDN
23	1333	96.9	1546	13	ADT90024	Adt90024 Human gen
24	1333	96.9	1546	13	ADT89914	Adt89914 Human gen
25	1333	96.9	1546	13	ADT90558	Adt90558 Human gen
26	1333	96.9	1546	13	ADT90145	Adt90145 Human gen
27	1333	96.9	1546	13	ADT90310	Adt90310 Human gen
28	1326	96.4	1981	2	AAV83711	Aav83711 Nucleic a
29	1253.6	91.2	1526	5	AAS73553	Aas73553 DNA encod
30	1214.4	88.3	1401	3	ABK12023	Abk12023 Human cyc
31	959.6	69.8	1247	6	ADH48825	Adh48825 NOV46 cod
32	933.8	67.9	1400	14	AEE14644	Aee14644 Hamster S
33	933.8	67.9	1403	14	AEE11002	Aee11002 Hamster c
34	653.6	47.5	826	3	AAZ58645	Aaz58645 Pancreati
35	653.6	47.5	826	14	ACL61419	ACL61419 Human col
36	559	40.7	572	3	ABK12024	Abk12024 Human cyc
37	507.2	36.9	525	4	AAH05869	Aah05869 Human cDN
38	493.4	35.9	694	13	ADQ55700	Adq55700 Novel can
39	485.6	35.3	497	3	AAC02111	Aac02111 Human sec
40	459.4	33.4	638	3	AAZ80102	Aaz80102 Human col
41	424.2	30.9	645	12	ADP28717	Adp28717 Human sec
42	424.2	30.9	849	5	AAS73552	Aas73552 DNA encod
43	424.2	30.9	849	12	ADP28716	Adp28716 Human sec
44	406.8	29.6	524	5	AAS73551	Aas73551 DNA encod
45	403	29.3	504	10	ADF79642	Adf79642 Leukaemia

## ALIGNMENTS

RESULT 1  
ADO26480



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1375	100.0	1375	2	AR448970	AR448970 Sequence
2	1345	97.8	1507	2	BD156255	BD156255 Primer fo
3	1345	97.8	1507	2	AX876674	AX876674 Sequence
4	1345	97.8	1507	5	AK001404	AK001404 Homo sapi
5	1345	97.8	1530	2	CQ959726	CQ959726 Sequence
6	1345	97.8	1530	2	CQ981348	CQ981348 Sequence
7	1345	97.8	1530	2	CS031177	CS031177 Sequence
8	1345	97.8	1530	2	CS040129	CS040129 Sequence
9	1345	97.8	1530	2	CS063038	CS063038 Sequence
10	1345	97.8	1530	2	CS080819	CS080819 Sequence
11	1345	97.8	1530	2	CS118908	CS118908 Sequence
12	1345	97.8	1530	2	CS161901	CS161901 Sequence
13	1345	97.8	1530	2	AR448968	AR448968 Sequence
14	1345	97.8	1530	2	AX779987	AX779987 Sequence
15	1329	96.7	1361	5	BC105086	BC105086 Homo sapi
16	1329	96.7	1361	5	BC105112	BC105112 Homo sapi
17	1326	96.4	1981	2	BD106750	BD106750 Cyclin-li
18	1312.4	95.4	1497	5	AK222611	AK222611 Homo sapi
19	1300.6	94.6	1551	5	AB168913	AB168913 Macaca fa
20	1300.4	94.6	1502	5	AF087910	AF087910 Homo sapi
21	1275.2	92.7	1496	5	AB169084	AB169084 Macaca fa
22	1266	92.1	1433	5	AB020981	AB020981 Homo sapi
23	1216	88.4	1401	5	AF002822	AF002822 Human cyc
24	1197	87.1	1206	5	CR533527	CR533527 Homo sapi
25	1195.4	86.9	1197	8	AY891143	AY891143 Synthetic
26	1195.4	86.9	1197	8	BT019457	BT019457 Synthetic
27	1193.8	86.8	1197	8	AY891142	AY891142 Synthetic
28	1193.8	86.8	1197	8	BT019456	BT019456 Synthetic
29	1192.2	86.7	1197	5	BT019458	BT019458 Homo sapi
30	1174	85.4	1342	2	CQ726844	CQ726844 Sequence
31	1034.6	75.2	1505	14	BT020648	BT020648 Bos tauru
32	1032.6	75.1	1465	14	BT021153	BT021153 Bos tauru
33	1032.4	75.1	1472	14	BT020669	BT020669 Bos tauru
34	1025.4	74.6	1454	14	BT020762	BT020762 Bos tauru
35	1021.4	74.3	1452	14	BT020822	BT020822 Bos tauru
36	1003.6	73.0	1446	14	BT021700	BT021700 Bos tauru
37	982.2	71.4	1299	14	AF080219	AF080219 Bos tauru
38	966.4	70.3	174811	5	AC147318	AC147318 Pan trogl
39	965	70.2	1520	6	BC088212	BC088212 Rattus no
40	965	70.2	1533	6	BC097952	BC097952 Rattus no
41	961.8	69.9	263877	12	AC128535	AC128535 Rattus no
c 42	961.8	69.9	312946	12	AC109691	AC109691 Rattus no
c 43	960.8	69.9	101768	5	AC006465	AC006465 Homo sapi
44	959.6	69.8	1247	2	AX921116	AX921116 Sequence
45	959.2	69.8	170513	12	AC023603	AC023603 Homo sapi

## ALIGNMENTS

RESULT 1  
AR448970



# SCORE Search Results Details for Application 10751380 and Search Result us-10-751-380-22.p2n.rni.

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 25, 2006, 23:43:04 ; Search time 256 Seconds  
(without alignments)  
4473.119 Million cell updates/sec

Title: US-10-751-380-22  
Perfect score: 2077  
Sequence: 1 EFGRKKRRQRMALLRRPTVS.....IPQLNSKAVKDLASPLIGRS 408

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10751380/runat\_25052006\_104509\_19740/app\_query.fasta\_1  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss02h -USER=US10751380\_CGN\_1\_1\_204@runat\_25052006\_104509\_19740  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2025	97.5	1375	3	US-10-083-889-21	Sequence 21, Appl
2	2025	97.5	1519	3	US-09-949-016-4357	Sequence 4357, Ap
3	2025	97.5	1530	3	US-10-083-889-1	Sequence 1, Appli
4	1090	52.5	826	3	US-09-337-171-12	Sequence 12, Appl
5	1090	52.5	826	3	US-09-773-459-12	Sequence 12, Appl
6	1028	49.5	1302	2	US-08-425-299A-1	Sequence 1, Appli
7	1028	49.5	1452	2	US-08-187-785-2	Sequence 2, Appli
8	1028	49.5	1452	3	US-09-023-655-1048	Sequence 1048, Ap
9	1028	49.5	1452	4	US-09-880-107-2308	Sequence 2308, Ap
10	1028	49.5	2122	3	US-09-949-016-3401	Sequence 3401, Ap
11	1000.5	48.2	1336	3	US-10-083-889-25	Sequence 25, Appl
12	777	37.4	23932	3	US-09-949-016-16099	Sequence 16099, A
13	748.5	36.0	638	3	US-09-328-111-186	Sequence 186, App
14	635	30.6	497	3	US-09-513-999C-2109	Sequence 2109, Ap
c 15	556	26.8	532	3	US-09-389-681-432	Sequence 432, App
c 16	556	26.8	532	3	US-09-620-405B-432	Sequence 432, App
c 17	556	26.8	532	3	US-09-433-826B-432	Sequence 432, App
c 18	556	26.8	532	3	US-09-604-287A-432	Sequence 432, App
c 19	556	26.8	532	3	US-09-834-759-432	Sequence 432, App
c 20	556	26.8	532	3	US-09-590-751A-432	Sequence 432, App
c 21	556	26.8	532	3	US-09-551-621-432	Sequence 432, App
c 22	556	26.8	532	3	US-09-551-621A-432	Sequence 432, App
c 23	556	26.8	532	3	US-10-076-622-432	Sequence 432, App
c 24	556	26.8	532	4	US-10-124-805-432	Sequence 432, App
25	547.5	26.4	1476	3	US-09-487-558B-77	Sequence 77, Appl
26	531.5	25.6	1636	3	US-09-496-444-1	Sequence 1, Appli
27	501.5	24.1	1497	3	US-09-248-796A-5917	Sequence 5917, Ap
28	497.5	24.0	1521	3	US-09-248-796A-1467	Sequence 1467, Ap
29	490	23.6	1618	3	US-09-684-169-1	Sequence 1, Appli
30	487.5	23.5	1752	2	US-08-463-090B-4	Sequence 4, Appli
31	482.5	23.2	15192	3	US-09-949-016-15143	Sequence 15143, A
32	475.5	22.9	1424	3	US-09-949-016-4092	Sequence 4092, Ap
33	475.5	22.9	1743	3	US-09-949-016-564	Sequence 564, App
34	443.5	21.4	2748	3	US-09-270-767-13675	Sequence 13675, A
35	424	20.4	1634	2	US-08-460-895-1	Sequence 1, Appli
36	424	20.4	1634	3	US-09-210-889-1	Sequence 1, Appli
37	424	20.4	1649	2	US-08-692-787-8	Sequence 8, Appli
38	424	20.4	1649	3	US-09-097-199-8	Sequence 8, Appli
39	424	20.4	1649	3	US-09-023-655-1268	Sequence 1268, Ap
40	424	20.4	2091	3	US-09-949-016-4548	Sequence 4548, Ap
41	348	16.8	345	3	US-09-016-434-679	Sequence 679, App
42	316	15.2	601	3	US-09-949-016-155713	Sequence 155713,

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 25, 2006, 23:12:04 ; Search time 675 Seconds  
(without alignments)  
6321.505 Million cell updates/sec

Title: US-10-751-380-22  
Perfect score: 2077  
Sequence: 1 EFGRKKRRQRMALLRRPTVS.....IPQLNSKAVKDLASPLIGRS 408

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10751380/runat\_25052006\_104502\_19637/app\_query.fasta\_1  
-DB=N\_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p  
-USER=US10751380\_@CGN\_1\_1\_1147\_@runat\_25052006\_104502\_19637 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*

2: geneseqn1990s:\*  
 3: geneseqn2000s:\*  
 4: geneseqn2001as:\*  
 5: geneseqn2001bs:\*  
 6: geneseqn2002as:\*  
 7: geneseqn2002bs:\*  
 8: geneseqn2003as:\*  
 9: geneseqn2003bs:\*  
 10: geneseqn2003cs:\*  
 11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*  
 14: geneseqn2005s:\*  
 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2025	97.5	1375	12	ADO26480	Ado26480 Chimeric
2	2025	97.5	1375	12	ADQ60193	Adq60193 Human cyc
3	2025	97.5	1507	4	AAH14263	Aah14263 Human cDN
4	2025	97.5	1507	12	ADQ19677	Adq19677 Human sof
5	2025	97.5	1530	10	ADF81588	Adf81588 Leukaemia
6	2025	97.5	1530	11	ADN95276	Adn95276 Human BEC
7	2025	97.5	1530	12	ADO26460	Ado26460 Human cyc
8	2025	97.5	1530	12	ADN03889	Adn03889 Antipsori
9	2025	97.5	1530	12	ADQ09231	Adq09231 Human CCN
10	2025	97.5	1530	12	ADQ60173	Adq60173 Human cDN
11	2025	97.5	1530	13	ADR25214	Adr25214 Breast ca
12	2025	97.5	1530	13	ACN39816	Acn39816 Tumour-as
13	2025	97.5	1530	13	ADU05981	Adu05981 Novel bro
14	2025	97.5	1530	14	ADY14877	Ady14877 DNA encod
15	2025	97.5	1530	14	ADY61817	Ady61817 Human gen
16	2025	97.5	1530	14	ADZ09578	Adz09578 Human bre
17	2025	97.5	1530	14	AEC82574	Aec82574 Breast ca
18	2025	97.5	1530	14	AEC75991	Aec75991 Genetic m
19	2025	97.5	1530	15	AEE84832	Aee84832 IMPDH mar
20	2025	97.5	1532	9	ACH03960	Ach03960 Human cDN
21	2025	97.5	1546	13	ADT90024	Adt90024 Human gen
22	2025	97.5	1546	13	ADT89914	Adt89914 Human gen
23	2025	97.5	1546	13	ADT90558	Adt90558 Human gen
24	2025	97.5	1546	13	ADT90145	Adt90145 Human gen
25	2025	97.5	1546	13	ADT90310	Adt90310 Human gen
26	2025	97.5	1981	2	AAV83711	Aav83711 Nucleic a
27	2025	97.5	2103	12	ADQ23839	Adq23839 Human sof
28	2019	97.2	1401	3	ABK12023	Abk12023 Human cyc
29	2019	97.2	1553	3	AAC77911	Aac77911 Human can
30	1922.5	92.6	1526	5	AAS73553	Aas73553 DNA encod
31	1780	85.7	1400	14	AEE14644	Aee14644 Hamster S
32	1780	85.7	1403	14	AEE11002	Aee11002 Hamster c
33	1605.5	77.3	1247	6	ADH48825	Adh48825 NOV46 cod
34	1090	52.5	826	3	AAZ58645	Aaz58645 Pancreati
35	1090	52.5	826	14	ACL61419	ACL61419 Human col
36	1028.5	49.5	7477	8	ACC44992	Acc44992 Vector pC
37	1028.5	49.5	7477	9	ADB85371	Adb85371 Vector DN

**SCORE Search Results Details for Application 10751380 and Search Result us-10-751-380-21.rnpbn.**

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<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10751380 and Search Result us-10-751-380-21.rnpbn.

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OM nucleic - nucleic search, using sw model

```
Run on:      May 25, 2006, 23:06:04 ; Search time 58 Seconds
              (without alignments)
              2676.139 Million cell updates/sec
```

```
Title:          US-10-751-380-21
Perfect score:  1375
Sequence:       1  gaattcgccaggaagaagcg.....cactgataggaagggtcctag 1375
```

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Published_Applications_NA_New:*
1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	$\frac{2}{3}$ Query
--------	------------------------

No.	Score	Match	Length	DB	ID	Description
1	1345	97.8	1530	6	US-10-505-928-198	Sequence 198, App
2	359.6	26.2	1452	6	US-10-505-928-318	Sequence 318, App
3	148.6	10.8	975	7	US-11-217-529-80034	Sequence 80034, A
4	147.6	10.7	1425	7	US-11-217-529-997	Sequence 997, App
5	144.2	10.5	954	7	US-11-217-529-4737	Sequence 4737, Ap
6	139.6	10.2	1284	7	US-11-217-529-75842	Sequence 75842, A
7	129	9.4	1287	7	US-11-217-529-347	Sequence 347, App
8	125.2	9.1	1473	7	US-11-217-529-2706	Sequence 2706, Ap
9	124	9.0	1743	7	US-11-145-307A-42	Sequence 42, Appl
10	118.2	8.6	1833	6	US-10-953-349-13178	Sequence 13178, A
11	116.4	8.5	1047	7	US-11-217-529-81613	Sequence 81613, A
12	116	8.4	1308	7	US-11-217-529-79016	Sequence 79016, A
13	106.8	7.8	1682	6	US-10-505-928-364	Sequence 364, App
14	99.2	7.2	1143	7	US-11-217-529-4165	Sequence 4165, Ap
15	92.2	6.7	1518	6	US-10-953-349-14536	Sequence 14536, A
16	90	6.5	1272	7	US-11-217-529-3381	Sequence 3381, Ap
17	86	6.3	1032	7	US-11-217-529-82400	Sequence 82400, A
18	79.2	5.8	1143	7	US-11-217-529-76758	Sequence 76758, A
19	71.6	5.2	2536	6	US-10-505-928-138	Sequence 138, App
20	36.4	2.6	969	7	US-11-217-529-78386	Sequence 78386, A
21	35.2	2.6	2568	7	US-11-217-529-5029	Sequence 5029, Ap
22	34.6	2.5	50000	6	US-10-528-659-2	Sequence 2, Appli
23	33.6	2.4	642	6	US-10-953-349-25936	Sequence 25936, A
c 24	33.6	2.4	1605	6	US-10-953-349-7721	Sequence 7721, Ap
c 25	33.6	2.4	1989	7	US-11-217-529-3335	Sequence 3335, Ap
c 26	33.2	2.4	413	7	US-11-301-554-1761	Sequence 1761, Ap
27	33.2	2.4	724	6	US-10-488-619-1649	Sequence 1649, Ap
28	33.2	2.4	1526	7	US-11-301-554-1931	Sequence 1931, Ap
29	33.2	2.4	1836	7	US-11-301-554-1933	Sequence 1933, Ap
c 30	33.2	2.4	2289	6	US-10-953-349-12180	Sequence 12180, A
c 31	33	2.4	813	6	US-10-953-349-1283	Sequence 1283, Ap
32	32.6	2.4	498	7	US-11-217-529-82431	Sequence 82431, A
c 33	32.4	2.4	462	7	US-11-217-529-80561	Sequence 80561, A
34	32	2.3	1026	7	US-11-217-529-75867	Sequence 75867, A
35	32	2.3	4536	6	US-10-953-349-9730	Sequence 9730, Ap
36	31.6	2.3	435	6	US-10-473-173-442	Sequence 442, App
c 37	31.6	2.3	1347	7	US-11-217-529-76835	Sequence 76835, A
38	31.6	2.3	2310	7	US-11-217-529-78545	Sequence 78545, A
c 39	31.4	2.3	1627	6	US-10-953-349-24356	Sequence 24356, A
40	31.2	2.3	963	7	US-11-217-529-5170	Sequence 5170, Ap
c 41	31.2	2.3	1379	6	US-10-953-349-30009	Sequence 30009, A
42	31.2	2.3	1592	6	US-10-953-349-36396	Sequence 36396, A
43	31	2.3	1126	6	US-10-953-349-3344	Sequence 3344, Ap
44	31	2.3	1711	7	US-11-270-287-2	Sequence 2, Appli
c 45	31	2.3	2159	6	US-10-953-349-2277	Sequence 2277, Ap

## ALIGNMENTS

## RESULT 1

US-10-505-928-198

; Sequence 198, Application US/10505928

; Publication No. US20060088532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

# SCORE Search Results Details for Application 10751380 and Search Result us-10-751-380-21.rni.

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OM nucleic - nucleic search, using sw model

Run on: May 25, 2006, 23:01:34 ; Search time 251 Seconds  
(without alignments)  
10250.098 Million cell updates/sec

Title: US-10-751-380-21  
Perfect score: 1375  
Sequence: 1 gaattcgccaggaagaagcg.....cactgataggaagggtcctag 1375

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1375	100.0	1375	3	US-10-083-889-21	Sequence 21, Appl
2	1345	97.8	1519	3	US-09-949-016-4357	Sequence 4357, Ap
3	1345	97.8	1530	3	US-10-083-889-1	Sequence 1, Appli
4	653.6	47.5	826	3	US-09-337-171-12	Sequence 12, Appl
5	653.6	47.5	826	3	US-09-773-459-12	Sequence 12, Appl
6	485.6	35.3	497	3	US-09-513-999C-2109	Sequence 2109, Ap
7	459.4	33.4	638	3	US-09-328-111-186	Sequence 186, App
8	361.2	26.3	1302	2	US-08-425-299A-1	Sequence 1, Appli
9	359.6	26.2	1452	2	US-08-187-785-2	Sequence 2, Appli
10	359.6	26.2	1452	3	US-09-023-655-1048	Sequence 1048, Ap
11	359.6	26.2	1452	4	US-09-880-107-2308	Sequence 2308, Ap
12	359.6	26.2	2122	3	US-09-949-016-3401	Sequence 3401, Ap
13	343	24.9	345	3	US-09-016-434-679	Sequence 679, App
14	324.2	23.6	1336	3	US-10-083-889-25	Sequence 25, Appl
15	241.2	17.5	23932	3	US-09-949-016-16099	Sequence 16099, A
c 16	216.4	15.7	532	3	US-09-389-681-432	Sequence 432, App
c 17	216.4	15.7	532	3	US-09-620-405B-432	Sequence 432, App
c 18	216.4	15.7	532	3	US-09-433-826B-432	Sequence 432, App
c 19	216.4	15.7	532	3	US-09-604-287A-432	Sequence 432, App
c 20	216.4	15.7	532	3	US-09-834-759-432	Sequence 432, App
c 21	216.4	15.7	532	3	US-09-590-751A-432	Sequence 432, App
c 22	216.4	15.7	532	3	US-09-551-621-432	Sequence 432, App
c 23	216.4	15.7	532	3	US-09-551-621A-432	Sequence 432, App
c 24	216.4	15.7	532	3	US-10-076-622-432	Sequence 432, App
c 25	216.4	15.7	532	4	US-10-124-805-432	Sequence 432, App
26	176.2	12.8	601	3	US-09-949-016-155713	Sequence 155713,
27	171.2	12.5	1476	3	US-09-487-558B-77	Sequence 77, Appl
28	160.2	11.7	1636	3	US-09-496-444-1	Sequence 1, Appli
29	145.2	10.6	1497	3	US-09-248-796A-5917	Sequence 5917, Ap
30	130.4	9.5	601	3	US-09-949-016-155709	Sequence 155709,
31	124	9.0	1424	3	US-09-949-016-4092	Sequence 4092, Ap
32	124	9.0	1743	3	US-09-949-016-564	Sequence 564, App
33	123	8.9	1618	3	US-09-684-169-1	Sequence 1, Appli
34	116.8	8.5	1521	3	US-09-248-796A-1467	Sequence 1467, Ap
35	112	8.1	1752	2	US-08-463-090B-4	Sequence 4, Appli
c 36	111	8.1	284	4	US-09-880-107-1072	Sequence 1072, Ap
37	108.2	7.9	15192	3	US-09-949-016-15143	Sequence 15143, A
38	106.8	7.8	1634	2	US-08-460-895-1	Sequence 1, Appli
39	106.8	7.8	1634	3	US-09-210-889-1	Sequence 1, Appli
40	106.8	7.8	1649	2	US-08-692-787-8	Sequence 8, Appli
41	106.8	7.8	1649	3	US-09-097-199-8	Sequence 8, Appli
42	106.8	7.8	1649	3	US-09-023-655-1268	Sequence 1268, Ap
43	106.8	7.8	2091	3	US-09-949-016-4548	Sequence 4548, Ap
44	101.4	7.4	1212	2	US-09-092-770-18	Sequence 18, Appl
45	101.4	7.4	1212	3	US-09-222-851-18	Sequence 18, Appl

## ALIGNMENTS

## RESULT 1

US-10-083-889-21

; Sequence 21, Application US/10083889

; Patent No. 6673894

; GENERAL INFORMATION:

; APPLICANT: Zahner, Joseph E.

; TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.